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<212> PRT
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508

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<220>
<223> Modified Env
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1	25	1.0	1.0	10	10	0.10	0.00	0.00
2	25	1.0	1.0	20	20	0.20	0.00	0.00
3	25	1.0	1.0	30	30	0.30	0.00	0.00
4	25	1.0	1.0	40	40	0.40	0.00	0.00
5	25	1.0	1.0	50	50	0.50	0.00	0.00
6	25	1.0	1.0	60	60	0.60	0.00	0.00
7	25	1.0	1.0	70	70	0.70	0.00	0.00
8	25	1.0	1.0	80	80	0.80	0.00	0.00
9	25	1.0	1.0	90	90	0.90	0.00	0.00
10	25	1.0	1.0	100	100	1.00	0.00	0.00

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[illegible]

<223> Modified Env/Tat from strain BH10

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<212> DNA
<213> Artificial sequence
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<210> 25
 <211> 108
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 25
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<210> 26
 <211> 105
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 26
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 tatgcaacag gtgatataat aggggatata agacaagcac attgt 105

<210> 27
 <211> 105
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 27
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 tatgcaacag gagaaataat aggagatata agacaagcac attgt 105

<210> 28
 <211> 102
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 28
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<210> 29
 <211> 105
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 29
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<210> 30
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 <212> DNA
 <213> Human immunodeficiency virus type 1

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<210> 31
 <211> 105
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 31
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 <211> 2562
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Env with multi-clade V3 loops

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Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile 245 250 255		
Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Leu Gly Cys Thr Arg 260 265 270		
Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr 275 280 285		
Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys 290 295 300		
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro 305 310 315 320		
Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln 325 330 335		
Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile Arg Gln Arg Thr Pro 340 345 350		
Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg Arg Ile Glu Asp Ile 355 360 365		
Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr Asn Thr Arg Thr Ser 370 375 380		
Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr 385 390 395 400		
Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys Thr Arg Pro Asn Asn 405 410 415		
Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly Arg Val Phe Tyr Thr 420 425 430		
Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala His Cys Cys Thr Arg 435 440 445		

Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
450 455 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465 470 475 480

Leu Gly Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Lys Gln Ile
485 490 495

Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe
500 505 510

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn
515 520 525

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
530 535 540

Thr Trp Phe Asn Ser Thr Trp Ser Thr Lys Gly Ser Asn Asn Thr Glu
545 550 555 560

Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn
565 570 575

Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly
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Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp
595 600 605

Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe Arg Pro Gly Gly Gly
610 615 620

Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val
625 630 635 640

Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val
645 650 655

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Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val
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<211> 1179
<212> DNA
<213> Human immunodeficiency virus type 1
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205

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
35 40 45

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tactaa 486

<210> 42
<211> 615
<212> DNA
<213> Human immunodeficiency virus type 1

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atcccgaggg gataa 615

<210> 43
<211> 132
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 43

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn Tyr Leu
 130 135 140

Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala
 145 150 155 160

Val Leu Ser Val Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser
 165 170 175

Phe Gln Thr His Leu Pro Ile Pro Arg Gly
 180 185

<210> 46
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 <212> DNA
 <213> Human immunodeficiency virus type 1

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<210> 47
 <211> 786
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 47
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Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg
35 40 45

Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln
65 70 75 80

Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg
100 105 110

Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu
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Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln
130 135 140

Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr
145 150 155 160

Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser
165 170 175

Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg
180 185 190

gaccaggaca agtattctat agaacaggag acataacagg agatataaga aaagcatatt 2340
gtggatcctg tacaagaccc aacaacaata caagaaaaag aatatcttta ggaccaggac 2400
gagtatttta tacagcagga gaaataatag gagacatcag aaaggcacat tgttgtagca 2460
gacctataaa caatacaaga aaaagtataa cttttgcacc aggacaagcg ctctatgcaa 2520
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<220>
<223> Modified Env/Tat

<400> 53

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Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly
115 120 125

Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
130 135 140

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
145 150 155 160

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
165 170 175

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
180 185 190

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
195 200 205

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
210 215 220

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
225 230 235 240

FOR INFORMATION

Leu Gly Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile
485 490 495

Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
500 505 510

Arg Gln Ala His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser
515 520 525

Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile
530 535 540

Gly Asp Ile Arg Gln Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile
545 550 555 560

Arg Gln Arg Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg
565 570 575

Arg Ile Glu Asp Ile Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr
580 585 590

Asn Thr Arg Thr Ser Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg
595 600 605

Thr Gly Asp Ile Thr Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys
610 615 620

Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly
625 630 635 640

Arg Val Phe Tyr Thr Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala
645 650 655

His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe
660 665 670

Ala Pro Gly Gln Ala Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
675 680 685

Arg Gln Ala His Cys Leu Gly Asn Ile Ser Arg Ala Lys Trp Asn Asn
690 695 700

Thr Leu Lys Gln Ile Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn
705 710 715 720

965	Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu	970	975
	980	985	990
	Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile		
	995	1000	1005
	Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu		
	1010	1015	1020
	Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr		
	1025	1030	1035
	Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile Val Gly Gly		
	1040	1045	1050
	Leu Val Gly Leu Arg Ile Val Phe Ala Thr His Leu Pro Ile Pro		
	1055	1060	1065
	Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu		
	1070	1075	1080
	Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser Leu Ala		
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	Leu Ile Trp		
	1100		
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	gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg	180	
	ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg gcaggaagaa	240	
	gcggagacag cgacgaagac ctctcaagg cagtcagact catcaagttt ctctatcaaa	300	
	gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc	360	
	aataataata gcaatagttg tgtggtccat agtaatcata gaatatagga aaatattaag	420	

195	200	205
Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu 210 215 220		
Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg 225 230 235 240		
Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile 245 250 255		
Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Leu Gly Cys Thr Arg 260 265 270		
Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr 275 280 285		
Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys 290 295 300		
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro 305 310 315 320		
Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln 325 330 335		
Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile Arg Gln Arg Thr Pro 340 345 350		
Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg Arg Ile Glu Asp Ile 355 360 365		
Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr Asn Thr Arg Thr Ser 370 375 380		
Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr 385 390 395 400		
Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys Thr Arg Pro Asn Asn 405 410 415		
Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly Arg Val Phe Tyr Thr 420 425 430		
Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala His Cys Cys Thr Arg 435 440 445		

Arg	Gln	Ala	His	Cys	Leu	Gly	Asn	Ile	Ser	Arg	Ala	Lys	Trp	Asn	Asn	
690						695					700					
Thr	Leu	Lys	Gln	Ile	Asp	Ser	Lys	Leu	Arg	Glu	Gln	Phe	Gly	Asn	Asn	
705					710					715					720	
Lys	Thr	Ile	Ile	Phe	Lys	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	
				725					730					735		
Thr	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asn	Ser	Thr	
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Gln	Leu	Phe	Asn	Ser	Thr	Trp	Phe	Asn	Ser	Thr	Trp	Ser	Thr	Lys	Gly	
		755					760					765				
Ser	Asn	Asn	Thr	Glu	Gly	Ser	Asp	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	
770						775					780					
Lys	Gln	Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	
785					790					795					800	
Pro	Pro	Ile	Ser	Gly	Gln	Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	
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			820					825					830			
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Lys	Tyr	Lys	Val	Val	Lys	Ile	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Lys	
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Gln	Gln	Asn	Asn	Leu	Leu	Arg	Ala	Ile	Glu	Ala	Gln	Gln	His	Leu	Leu	
		915					920					925				

[illegible]

335

Gln Ile Leu Ile Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu
565 570 575

Case	Age	Sex	Duration of illness	Onset	Course	Outcome
1	25	M	10 years	Acute	Chronic	Recovery
2	30	F	5 years	Subacute	Chronic	Recovery
3	35	M	15 years	Acute	Chronic	Recovery
4	40	F	20 years	Subacute	Chronic	Recovery
5	45	M	25 years	Acute	Chronic	Recovery
6	50	F	30 years	Subacute	Chronic	Recovery
7	55	M	35 years	Acute	Chronic	Recovery
8	60	F	40 years	Subacute	Chronic	Recovery
9	65	M	45 years	Acute	Chronic	Recovery
10	70	F	50 years	Subacute	Chronic	Recovery
11	75	M	55 years	Acute	Chronic	Recovery
12	80	F	60 years	Subacute	Chronic	Recovery
13	85	M	65 years	Acute	Chronic	Recovery
14	90	F	70 years	Subacute	Chronic	Recovery
15	95	M	75 years	Acute	Chronic	Recovery

<213> Artificial sequence
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 <212> DNA
 <213> Artificial sequence
 <220>
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 <210> 66
 <211> 36
 <212> DNA
 <213> Artificial sequence
 <220>
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 <400> 66
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 <211> 47
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 <213> Artificial sequence

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 <213> Artificial sequence

<220>
 <223> MMLV SD site

<400> 72
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<210> 73
 <211> 9
 <212> DNA
 <213> Artificial sequence

<220>
 <223> MMLV SA site

<400> 73
 ctgctgcag 9

<210> 74
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 <212> DNA
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